



1

SEQUENCE LISTING

<110> HAMILTON, STEPHEN

<120> ENDOMANNOSIDASES IN THE MODIFICATION OF GLYCOPROTEINS  
IN EUKARYOTES

<130> GFI/109 CIP

<140> 10/695,243

<141> 2003-10-27

<150> 10/371,877

<151> 2003-02-20

<160> 29

<170> PatentIn Ver. 3.2

<210> 1

<211> 1389

<212> DNA

<213> Homo sapiens

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<221> CDS

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Leu Phe Ile Phe Ser Leu Met Met Gly Leu Lys Met Leu Arg Pro Asn	
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Thr Ala Thr Phe Gly Ala Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu	
35 40 45	

cat caa cga act att cat ttg ggg aaa aat ttt gat ttc caa aag agt	192
His Gln Arg Thr Ile His Leu Gly Lys Asn Phe Asp Phe Gln Lys Ser	
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gac aga atc aac agt gaa aca aat acc aag aat tta aaa agt gtt gaa	240
Asp Arg Ile Asn Ser Glu Thr Asn Thr Lys Asn Leu Lys Ser Val Glu	
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atc act atg aaa cct tcc aaa gcc tct gaa ctt aac ttg gat gaa cta	288
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Pro Pro Leu Asn Asn Tyr Leu His Val Phe Tyr Tyr Ser Trp Tyr Gly	
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aat cca caa ttt gat ggt aaa tat ata cat tgg aat cat cca gtg tta	384
Asn Pro Gln Phe Asp Gly Lys Tyr Ile His Trp Asn His Pro Val Leu	
115 120 125	
gag cat tgg gac cct aga ata gcc aag aat tat cca caa ggg aga cac	432
Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr Pro Gln Gly Arg His	
130 135 140	
aac cct cca gat gac att ggc tcc agc ttt tat cct gaa ttg gga agt	480
Asn Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr Pro Glu Leu Gly Ser	
145 150 155 160	
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Tyr Ser Ser Arg Asp Pro Ser Val Ile Glu Thr His Met Arg Gln Met	
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cgc tca gct tca att ggt gta cta gcc ctg tct tgg tac cca cct gat	576
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180 185 190	
gta aat gat gaa aat gga gaa cct act gat aac ttg gta ccc act att	624
Val Asn Asp Glu Asn Gly Glu Pro Thr Asp Asn Leu Val Pro Thr Ile	
195 200 205	
ttg gat aaa gct cat aaa tat aac cta aag gtt act ttt cac ata gaa	672
Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val Thr Phe His Ile Glu	
210 215 220	
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Lys Thr Gly Asn Ala Leu Pro Met Phe Tyr Val Tyr Asp Ser Tyr Ile	
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 325 330 335

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 Gly Leu Ser Ala Ala Leu Gln Thr Arg Pro Ser Leu Ile Ser Ile Thr  
 385 390 395 400

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 405 410 415

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&lt;210&gt; 2

&lt;211&gt; 462

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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Thr Ala Thr Phe Gly Ala Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu  
 35 40 45  
 His Gln Arg Thr Ile His Leu Gly Lys Asn Phe Asp Phe Gln Lys Ser  
 50 55 60  
 Asp Arg Ile Asn Ser Glu Thr Asn Thr Lys Asn Leu Lys Ser Val Glu  
 65 70 75 80  
 Ile Thr Met Lys Pro Ser Lys Ala Ser Glu Leu Asn Leu Asp Glu Leu  
 85 90 95  
 Pro Pro Leu Asn Asn Tyr Leu His Val Phe Tyr Tyr Ser Trp Tyr Gly  
 100 105 110  
 Asn Pro Gln Phe Asp Gly Lys Tyr Ile His Trp Asn His Pro Val Leu  
 115 120 125  
 Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr Pro Gln Gly Arg His  
 130 135 140  
 Asn Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr Pro Glu Leu Gly Ser  
 145 150 155 160  
 Tyr Ser Ser Arg Asp Pro Ser Val Ile Glu Thr His Met Arg Gln Met  
 165 170 175  
 Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser Trp Tyr Pro Pro Asp  
 180 185 190  
 Val Asn Asp Glu Asn Gly Glu Pro Thr Asp Asn Leu Val Pro Thr Ile  
 195 200 205  
 Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val Thr Phe His Ile Glu  
 210 215 220  
 Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met Tyr Lys Asn Val Lys Tyr  
 225 230 235 240  
 Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe Tyr Arg Tyr Lys Thr  
 245 250 255  
 Lys Thr Gly Asn Ala Leu Pro Met Phe Tyr Val Tyr Asp Ser Tyr Ile  
 260 265 270  
 Thr Lys Pro Glu Lys Trp Ala Asn Leu Leu Thr Thr Ser Gly Ser Arg  
 275 280 285  
 Ser Ile Arg Asn Ser Pro Tyr Asp Gly Leu Phe Ile Ala Leu Leu Val  
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<222> (1) .. (1386)
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Leu	Phe	Ile	Phe	Ser	Leu	Met	Met	Gly	Leu	Lys	Met	Leu	Trp	Pro	Asn		
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Met	Thr	Val	Leu	Pro	Ala	Lys	Ala	Ser	Glu	Val	Asn	Leu	Glu	Glu	Leu	
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Ser	Arg	Asp	Asp	Asn	Gly	Glu	Ala	Thr	Asp	His	Leu	Val	Pro	Thr	Ile	
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Leu	Asp	Lys	Ala	His	Lys	Tyr	Asn	Leu	Lys	Val	Thr	Phe	His	Ile	Glu	
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Ile	Ile	Asp	Lys	Tyr	Gly	Asn	His	Pro	Ala	Phe	Tyr	Arg	Tyr	Lys	Thr	
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Arg	Thr	Gly	His	Ser	Leu	Pro	Met	Phe	Tyr	Val	Tyr	Asp	Ser	Tyr	Ile	
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275 280 285	
agt gtt cgc agt tct ctt tat gat gga ttg ttt att gca ctt cta gta	912
Ser Val Arg Ser Ser Leu Tyr Asp Gly Leu Phe Ile Ala Leu Leu Val	
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gaa gaa aag cat aaa aat gat att ctt cag agt ggt ttt gat ggt att	960
Glu Glu Lys His Lys Asn Asp Ile Leu Gln Ser Gly Phe Asp Gly Ile	
305 310 315 320	
tac aca tat ttt gcc aca aat ggc ttt aca tat ggc tca tct cat cag	1008
Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly Ser Ser His Gln	
325 330 335	
aat tgg aat aac ctg aaa tcc ttt tgt gaa aag aac aac ttg atg ttt	1056
Asn Trp Asn Asn Leu Lys Ser Phe Cys Glu Lys Asn Asn Leu Met Phe	
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370 375 380	
ggt cta agt gct gca ctc cag acc cac ccc agt tta att tcc atc acc	1200
Gly Leu Ser Ala Ala Leu Gln Thr His Pro Ser Leu Ile Ser Ile Thr	
385 390 395 400	
tct ttc aat gag tgg cat gaa gga act caa att gaa aag gct gtc ccc	1248
Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu Lys Ala Val Pro	
405 410 415	
aaa aga act gct aac acg ata tac ctg gat tac cgg cct cat aag cca	1296
Lys Arg Thr Ala Asn Thr Ile Tyr Leu Asp Tyr Arg Pro His Lys Pro	
420 425 430	
agt ctt tat cta gaa cta act cga aag tgg tct gaa aaa ttc agt aag	1344
Ser Leu Tyr Leu Glu Leu Thr Arg Lys Trp Ser Glu Lys Phe Ser Lys	
435 440 445	
gaa aga atg acg tat gca ttg gat caa cag cag cct gct tca taa	1389
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&lt;210&gt; 4

&lt;211&gt; 462

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 4

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Ala	Ala	Ser	Phe	Gly	Pro	Pro	Phe	Gly	Leu	Asp	Leu	Leu	Pro	Glu	Leu	
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His	Pro	Leu	Asn	Ala	His	Ser	Gly	Asn	Lys	Ala	Asp	Phe	Gln	Arg	Ser	
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Asp	Arg	Ile	Asn	Met	Glu	Thr	Asn	Thr	Lys	Ala	Leu	Lys	Gly	Ala	Gly	
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Pro	Pro	Leu	Asn	Tyr	Phe	Leu	His	Ala	Phe	Tyr	Tyr	Ser	Trp	Tyr	Gly	
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Asn	Pro	Gln	Phe	Asp	Gly	Lys	Tyr	Ile	His	Trp	Asn	His	Pro	Val	Leu	
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Glu	His	Trp	Asp	Pro	Arg	Ile	Ala	Lys	Asn	Tyr	Pro	Gln	Gly	Gln	His	
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Ser	Pro	Pro	Asp	Asp	Ile	Gly	Ser	Ser	Phe	Tyr	Pro	Glu	Leu	Gly	Ser	
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Pro	Tyr	Ser	Asn	Arg	Asp	Asp	Gln	Asn	Met	His	Gln	Asn	Ile	Lys	Tyr	
225					230					235					240	
Ile	Ile	Asp	Lys	Tyr	Gly	Asn	His	Pro	Ala	Phe	Tyr	Arg	Tyr	Lys	Thr	
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Thr	Lys	Pro	Thr	Ile	Trp	Ala	Asn	Leu	Leu	Thr	Pro	Ser	Gly	Ser	Gln	
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Ser Val Arg Ser Ser Leu Tyr Asp Gly Leu Phe Ile Ala Leu Leu Val  
 290 295 300

Glu Glu Lys His Lys Asn Asp Ile Leu Gln Ser Gly Phe Asp Gly Ile  
 305 310 315 320

Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly Ser Ser His Gln  
 325 330 335

Asn Trp Asn Asn Leu Lys Ser Phe Cys Glu Lys Asn Asn Leu Met Phe  
 340 345 350

Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser Ile Arg Pro Trp  
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Asn Thr Gln Asn Thr Arg Asn Arg Val Asn Gly Lys Tyr Tyr Glu Val  
 370 375 380

Gly Leu Ser Ala Ala Leu Gln Thr His Pro Ser Leu Ile Ser Ile Thr  
 385 390 395 400

Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu Lys Ala Val Pro  
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Lys Arg Thr Ala Asn Thr Ile Tyr Leu Asp Tyr Arg Pro His Lys Pro  
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Ser Leu Tyr Leu Glu Leu Thr Arg Lys Trp Ser Glu Lys Phe Ser Lys  
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<223> Description of Artificial Sequence: Synthetic primer

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<211> 59

<212> DNA

<213> Artificial Sequence

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<212> DNA

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<212> DNA

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<223> Description of Artificial Sequence: Synthetic primer

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<210> 21

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<212> DNA

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<223> Description of Artificial Sequence: Synthetic primer

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&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic primer

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40

&lt;210&gt; 23

&lt;211&gt; 290

&lt;212&gt; PRT

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&lt;400&gt; 23

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85 90 95Asp Ser Tyr Ile Thr Lys Pro Lys Thr Trp Ala Asn Leu Leu Thr Pro  
100 105 110Ser Gly Ser Gln Ser Val Arg Gly Ser Pro Tyr Asp Gly Leu Phe Ile  
115 120 125Ala Leu Leu Val Glu Glu Lys His Lys Tyr Asp Ile Leu Gln Ser Gly  
130 135 140Phe Asp Gly Ile Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly  
145 150 155 160Ser Ser His Gln Asn Trp Asn Lys Leu Lys Ser Phe Cys Glu Lys Asn  
165 170 175Asn Met Ile Phe Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser  
180 185 190Ile Arg Pro Trp Asn Thr Gln Asn Thr Arg Asn Arg Ile Asn Gly Lys  
195 200 205

Tyr Tyr Glu Val Gly Leu Ser Ala Ala Leu Gln Thr Gln Pro Ser Leu  
 210 215 220  
 Ile Ser Ile Thr Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu  
 225 230 235 240  
 Lys Ala Val Pro Lys Arg Thr Ala Asn Thr Val Tyr Leu Asp Tyr Arg  
 245 250 255  
 Pro His Lys Pro Ser Leu Tyr Leu Glu Ile Thr Arg Lys Trp Ser Glu  
 260 265 270  
 Lys Tyr Ser Lys Glu Arg Met Thr Tyr Ala Leu Asp Gln Gln Leu Pro  
 275 280 285  
 Ala Ser  
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<210> 24  
 <211> 290  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Met Arg Gln Met Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser Trp  
 1 5 10 15  
 Tyr Pro Pro Asp Val Asn Asp Glu Asn Gly Glu Pro Thr Asp Asn Leu  
 20 25 30  
 Val Pro Thr Ile Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val Thr  
 35 40 45  
 Phe His Ile Glu Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met Tyr Lys  
 50 55 60  
 Asn Val Lys Tyr Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe Tyr  
 65 70 75 80  
 Arg Tyr Lys Thr Lys Thr Gly Asn Ala Leu Pro Met Phe Tyr Val Tyr  
 85 90 95  
 Asp Ser Tyr Ile Thr Lys Pro Glu Lys Trp Ala Asn Leu Leu Thr Thr  
 100 105 110  
 Ser Gly Ser Arg Ser Ile Arg Asn Ser Pro Tyr Asp Gly Leu Phe Ile  
 115 120 125  
 Ala Leu Leu Val Glu Glu Lys His Lys Tyr Asp Ile Leu Gln Ser Gly  
 130 135 140  
 Phe Asp Gly Ile Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr Gly  
 145 150 155 160

Ser Ser His Gln Asn Trp Ala Ser Leu Lys Leu Phe Cys Asp Lys Tyr  
 165 170 175  
 Asn Leu Ile Phe Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr Ser  
 180 185 190  
 Ile Arg Pro Trp Asn Thr Gln Asn Thr Arg Asn Arg Ile Asn Gly Lys  
 195 200 205  
 Tyr Tyr Glu Ile Gly Leu Ser Ala Ala Leu Gln Thr Arg Pro Ser Leu  
 210 215 220  
 Ile Ser Ile Thr Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile Glu  
 225 230 235 240  
 Lys Ala Val Pro Lys Arg Thr Ser Asn Thr Val Tyr Leu Asp Tyr Arg  
 245 250 255  
 Pro His Lys Pro Gly Leu Tyr Leu Glu Leu Thr Arg Lys Trp Ser Glu  
 260 265 270  
 Lys Tyr Ser Lys Glu Arg Ala Thr Tyr Ala Leu Asp Arg Gln Leu Pro  
 275 280 285  
 Val Ser  
 290

<210> 25  
 <211> 195  
 <212> PRT  
 <213> Homo sapiens

<400> 25

Met Ala Lys Phe Arg Arg Arg Thr Cys Ile Ile Leu Ala Leu Phe Ile  
 1 5 10 15  
 Leu Phe Ile Phe Ser Leu Met Met Gly Leu Lys Met Leu Arg Pro Asn  
 20 25 30  
 Thr Ala Thr Phe Gly Ala Pro Phe Gly Leu Asp Leu Leu Pro Glu Leu  
 35 40 45  
 His Gln Arg Thr Ile His Leu Gly Lys Asn Phe Asp Phe Gln Lys Ser  
 50 55 60  
 Asp Arg Ile Asn Ser Glu Thr Asn Thr Lys Asn Leu Lys Ser Val Glu  
 65 70 75 80  
 Ile Thr Met Lys Pro Ser Lys Ala Ser Glu Leu Asn Leu Asp Glu Leu  
 85 90 95



Pro Pro Leu Asn Asn Tyr Leu His Val Phe Tyr Tyr Ser Trp Tyr Gly  
 100 105 110

Asn Pro Gln Phe Asp Gly Lys Tyr Ile His Trp Asn His Pro Val Leu  
 115 120 125

Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr Pro Gln Gly Arg His  
 130 135 140

Asn Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr Pro Glu Leu Gly Ser  
 145 150 155 160

Tyr Ser Ser Arg Asp Pro Ser Val Ile Glu Thr His Met Arg Gln Met  
 165 170 175

Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser Trp Tyr Pro Pro Asp  
 180 185 190

Val Asn Glu  
 195

<210> 26

<211> 451

<212> PRT

<213> Rattus norvegicus

<400> 26

Met Gly Ala Leu Met Ala Thr Tyr Ser Glu Gly Met Met Gly Cys Ser  
 1 5 10 15

Ser Val Gly Arg Cys Phe Ser Ser Thr Leu Ser Pro Ile Ile Thr Leu  
 20 25 30

Val Ala Thr Ser Met Lys Ser Thr Pro Arg Val Leu Glu Asn Lys Ala  
 35 40 45

Asp Phe Gln Arg Ser Asp Arg Ile Asp Met Glu Thr Asn Thr Lys Asp  
 50 55 60

Leu Lys Gly Ala Gly Val Thr Val His Pro Pro Arg Ala Ser Glu Val  
 65 70 75 80

Asn Leu Glu Glu Leu Pro Pro Leu Asn Tyr Phe Val His Ala Phe Tyr  
 85 90 95

Tyr Ser Trp Tyr Gly Asn Pro Gln Phe Asp Gly Lys Tyr Val His Trp  
 100 105 110

Asn His Pro Val Leu Glu His Trp Asp Pro Arg Ile Ala Lys Asn Tyr  
 115 120 125

Pro Gln Gly Arg His Ser Pro Pro Asp Asp Ile Gly Ser Ser Phe Tyr  
 130 135 140

Pro Glu Leu Gly Ser Tyr Ser Ser Arg Asp Pro Ser Val Ile Glu Thr  
 145 150 155 160  
 His Met Lys Gln Met Arg Ser Ala Ser Ile Gly Val Leu Ala Leu Ser  
 165 170 175  
 Trp Tyr Pro Pro Asp Ala Ser Asp Glu Asn Gly Glu Ala Thr Asp Tyr  
 180 185 190  
 Leu Val Pro Thr Ile Leu Asp Lys Ala His Lys Tyr Asn Leu Lys Val  
 195 200 205  
 Thr Phe His Ile Glu Pro Tyr Ser Asn Arg Asp Asp Gln Asn Met His  
 210 215 220  
 Gln Asn Val Lys Tyr Ile Ile Asp Lys Tyr Gly Asn His Pro Ala Phe  
 225 230 235 240  
 Tyr Arg Tyr Lys Thr Arg Met Gly His Ser Leu Pro Met Phe Tyr Ile  
 245 250 255  
 Tyr Asp Ser Tyr Ile Thr Lys Pro Lys Thr Trp Ala Asn Leu Leu Thr  
 260 265 270  
 Pro Ser Gly Ser Gln Ser Val Arg Gly Ser Pro Tyr Asp Gly Leu Phe  
 275 280 285  
 Ile Ala Leu Leu Val Glu Glu Lys His Lys Tyr Asp Ile Leu Gln Ser  
 290 295 300  
 Gly Phe Asp Gly Ile Tyr Thr Tyr Phe Ala Thr Asn Gly Phe Thr Tyr  
 305 310 315 320  
 Gly Ser Ser His Gln Asn Trp Asn Lys Leu Lys Ser Phe Cys Glu Lys  
 325 330 335  
 Asn Asn Met Ile Phe Ile Pro Ser Val Gly Pro Gly Tyr Ile Asp Thr  
 340 345 350  
 Ser Ile Arg Pro Trp Asn Thr Gln Asn Thr Arg Asn Arg Ile Asn Gly  
 355 360 365  
 Lys Tyr Tyr Glu Val Gly Leu Ser Ala Ala Leu Gln Thr Gln Pro Ser  
 370 375 380  
 Leu Ile Ser Ile Thr Ser Phe Asn Glu Trp His Glu Gly Thr Gln Ile  
 385 390 395 400  
 Glu Lys Ala Val Pro Lys Arg Thr Ala Asn Thr Val Tyr Leu Asp Tyr  
 405 410 415  
 Arg Pro His Lys Pro Ser Leu Tyr Leu Glu Ile Thr Arg Lys Trp Ser  
 420 425 430

Glu Lys Tyr Ser Lys Glu Arg Met Thr Tyr Ala Leu Asp Gln Gln Leu  
 435 440 445

Pro Ala Ser  
 450

<210> 27  
 <211> 9  
 <212> PRT  
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<220>  
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 peptide motif

<220>  
 <221> MOD\_RES  
 <222> (4)  
 <223> Lys or Arg

<400> 27  
 Asp Phe Gln Xaa Ser Asp Arg Ile Asn  
 1 5

<210> 28  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 peptide

<400> 28  
 His Asp Glu Leu  
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<210> 29  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 peptide

<400> 29  
 Lys Asp Glu Leu  
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